SEQUENCE LISTING

<110> Rosen, Craig A.
      Sadeghi, Homa
      Prior, Christopher P.
      Turner, Andrew J.

<120> Albumin Fusion Proteins

<130> PF543

<140> Unassigned
<141> 2001-04-12

<150> 60/229,358
<151> 2000-04-12

<150> 60/256,931
<151> 2000-12-21

<150> 60/199,384
<151> 2000-04-25

<160> 36

<170> PatentIn Ver. 2.1

<210> 1
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer useful to clone human growth hormone cDNA

<400> 1
cccaagaatt cccttatcca ggc   23

<210> 2
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> primer bind
<223> primer useful to clone human growth hormone cDNA

<400> 2
gggaagctta gaagccacag gatccctcca cag   33

<210> 3
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_structure

1

<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

<400> 3
gataaagatt cccaac   16

<210> 4
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments
with non cohesive ends.

<400> 4
aattgttggg aatcttt   17

<210> 5
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<221> misc structure
<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

<400> 5
ttaggcttat tcccaac   17

<210> 6
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA fragments
with non-cohesive ends.

<400> 6
aattgttggg aataagcc   18

<210> 7
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> 1)..(19)
<223> invertase leader sequence

<220>

<221> SITE
<222> 20)..(24)
<223> first 5 amino acids of mature human serum albumin

<400> 7
Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
1   5   10   15

Ile Ser Ala Asp Ala His Lys Ser
            20

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA
fragments with non-cohesive ends.

<400> 8
gagatgcaca cctgagtgag g   21

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA
fragments with non-cohesive ends.

<400> 9
gatcctgtgg cttcgatgca cacaaga   27

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> misc structure
<223> synthetic oligonucleotide used to join DNA
fragments with non cohesive ends.

<400> 10
ctcttgtgtg catcgaagcc acag   24

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

3

<221> misc_structure
<223> synthetic oligonucleotide used to join DNA
fragments with non-cohesive ends.

<400> 11
tgtggaagag cctcagaatt tattcccaac   30

<210> 12
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA
fragments with non cohesive ends.

<400> 12
aattgttggg aataaattct gaggctcttc c   31

<210> 13
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA
fragments with non-cohesive ends.

<400> 13
ttaggcttag gtggcggtgg atccggcggt ggtggatctt tcccaac   47

<210> 14
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<221> misc structure
<223> synthetic oligonucleotide used to join DNA
fragments with non-cohesive ends.

<400> 14
aattgttggg aaagatccac caccgccgga tccaccgcca cctaagcc   48

<210> 15
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_structure
<223> synthetic oligonucleotide used to join DNA
fragments with non-cohesive ends.

<400> 15
ttaggcttag gcggtgatgg atctggtggc ggcggatctg gtggcggtga atccttccca 60
ac 62

<210> 16
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<221> misc structure
<223> synthetic oligonucleotide used to join DNA
fragments with non cohesive ends.

<400> 16
aattgttggg aaggatccac cgccaccaga tccgccgcca ccagatccac caccgcctaa 60
gcc 63

<210> 17
<211> 1782
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1755)

<400> 17
gat gca cac aag agt gag gtt gct cat cgg ttt aaa gat ttg gga gaa   48
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1   5   10   15

gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag   96
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
                20   25   30

cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa   144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
            35   40   45

ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa   192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
        50   55   60

tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt   240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65   70   75   80

cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct   288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85   90   95

gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc   336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
                100   105   110

ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat   384

```
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115             120                 125

gat aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga   432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
        130             135                 140

aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg   480
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc   528
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg   576
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
                180                 185                 190

tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa   624
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
                195                 200                 205

aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc   672
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
        210                 215                 220

aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa   720
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225                 230                 235                 240

gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac   768
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc   816
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
                260                 265                 270

agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac   864
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
                275                 280                 285

tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca   912
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
        290                 295                 300

tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct   960
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga   1008
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

agg cat cct gat tac tct gtc gtg ctg ctg cta aga ctt gcc aag aca   1056
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
                340                 345                 350

tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa   1104
```
6

```
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Gln
        355               360               365

tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct  1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
        370               375               380

cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag  1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385               390               395               400

tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc  1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405               410               415

caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa  1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
                420               425               430

gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt  1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
                435               440               445

gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat  1392
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
                450               455               460

gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc  1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465               470               475               480

ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca  1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485               490               495

tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat  1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
                500               505               510

ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca  1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
                515               520               525

ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg  1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
                530               535               540

aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag  1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545               550               555               560

gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt  1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565               570               575

gct gca agt caa gct gcc tta ggc tta taacatctac atttaaaagc atctcag  1782
Ala Ala Ser Gln Ala Ala Leu Gly Leu
                580               585
```

7

<210> 18
<211> 585
<212> PRT
<213> Homo Sapiens

<400> 18
Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1   5   10   15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
                20   25   30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
            35   40   45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
        50   55   60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65   70   75   80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85   90   95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
                100   105   110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
            115   120   125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
            130   135   140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145   150   155   160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165   170   175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
                180   185   190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
            195   200   205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210   215   220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225   230   235   240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245   250   255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260   265   270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
            275   280   285

8

```
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
            355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
            435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
                500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
        530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
                580                 585


<210> 19
```

<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer used to generate XhoI and ClaI
site in pPPC0006

<400> 19
gcctcgagaa aagagatgca cacaagagtg aggttgctca tcgatttaaa gatttgg   57

<210> 20
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer used in generation XhoI and ClaI
site in pPPC0006

<400> 20
aatcgatgag caacctcact cttgtgtgca tctcttttct cgaggctcct ggaataag   58

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer used in generation XhoI and ClaI
site in pPPC0006

<400> 21
tacaaactta agagtccaat tagc   24

<210> 22
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer used in generation XhoI and ClaI
site in pPPC0006

<400> 22
cacttctcta gagtggtttc atatgtctt   29

<210> 23
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<221> Misc Structure
<223> Synthetic oligonucleotide used to alter restriction
sites in pPPC0007

<400> 23
aagctgcctt aggcttataa taaggcgcgc cggccggcca tttaaactaa gcttaattct 60

<210> 24
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<221> Misc Structure
<223> Synthetic oligonucleotide used to alter restriction
sites in pPPC0007

<400> 24
agaattaagc ttagtttaaa cggccggccg gcgcgcctta ttataagcct aaggcagctt 60

<210> 25
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of albumin
fusion protein in which the albumin moiety is N-terminal
of the Therapeutic Protein

<220>
<221> misc_feature
<222> (18)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (19)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (20)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (21)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<223> n equals a,t,g, or c

<220>
<221> misc_feature

<222> (23)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (24)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (25)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (26)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (27)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (28)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (30)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (31)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (32)
<223> n equals a,t,g, or c

<400> 25
aagctgcctt aggcttannn nnnnnnnnnn nn   32

<210> 26
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for generation of albumin
fusion protein in which the albumin moiety is N-terminal

12

of the Therapeutic Protein

<220>
<221> misc_feature
<222> (37)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (38)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (39)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (41)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (44)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (47)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (48)

<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (49)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (50)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (51)
<223> n equals a,t,g, or c

<400> 26
gcgcgcgttt aaacggccgg ccggcgcgcc ttattannnn nnnnnnnnnn n   51

<210> 27
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer useful for generation of albumin fusion
protein in which the albumin moiety is c terminal of the
Therapeutic Protein

<220>
<221> misc_feature
<222> (19)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (20)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (21)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (22)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (23)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (24)
<223> n equals a,t,g, or c

14

<220>
<221> misc_feature
<222> (25)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (26)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (27)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (28)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (30)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (31)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (32)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (33)
<223> n equals a,t,g, or c

<400> 27
aggagcgtcg acaaaagann nnnnnnnnnn nnn   33

<210> 28
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for generation of albumin
fusion protein in which the albumin moiety is c-terminal of
the Therapeutic Protein

15

<220>
<221> misc_feature
<222> (38)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (39)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (41)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (44)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (46)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (47)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (48)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (49)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (50)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (51)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (52)
<223> n equals a,t,g, or c

<400> 28
ctttaaatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnn nn   52

<210> 29
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> signal peptide of natural human serum albumin protein

<400> 29
Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
 1   5   10   15

Tyr Ser Arg Ser Leu Asp Lys Arg
            20

<210> 30
<211> 114
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of PC4:HSA
albumin fusion VECTOR

<220>
<221> misc_feature
<222> (5)..(10)
<223> BamHI retsriction site

<220>
<221> misc_feature
<222> (11)..(16)
<223> Hind III retsriction site

<220>
<221> misc_feature
<222> (17)..(27)
<223> Kozak sequence

17

<220>
<221> misc_feature
<222> (25)..(97)
<223> cds natural signal sequence of human serum albumin

<220>
<221> misc_feature
<222> (75)..(81)
<223> XhoI restriction site

<220>
<221> misc_feature
<222> (98)..(114)
<223> cds first six amino acids of human serum albumin

<400> 30
tcagggatcc aagcttccgc caccatgaag tgggtaacct ttatttcct tcttttctc 60

tttagctcgg cttactcgag gggtgtattt cgtcgagatg cacacaagag tgag   114

<210> 31
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for generation of
PC4:HSA albumin fusion VECTOR

<220>
<221> misc_feature
<222> (6)..(11)
<223> Asp718 restriction site

<220>
<221> misc_feature
<222> (12)..(17)
<223> EcoRI restriction site

<220>
<221> misc_feature
<222> (15)..(17)
<223> reverse complement of stop codon

<220>
<221> misc_feature
<222> (18)..(25)
<223> AscI restriction site

<220>
<221> misc_feature
<222> (18)..(43)
<223> reverse complement of DNA sequence encoding last 9 amino acids

<400> 31
gcagcggtac cgaattcggc gcgccttata agcctaaggc agc   43

18

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for inserting Therapeutic
protein into pC4:HSA vector

<220>
<221> misc_feature
<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (30)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (31)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (32)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (33)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (34)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (35)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (36)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (37)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (38)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (39)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (41)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (44)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (46)
<223> n equals a,t,g, or c

<400> 32
ccgccgctcg aggggtgtgt ttcgtcgann nnnnnnnnnn nnnnnn   46

<210> 33
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for inserting Therapeutic
protein into pC4:HSA vector

<220>
<221> misc_feature
<222> (38)
<223> n equals a,t,g, or c

<220>
<221> misc_feature

20

<222> (39)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (41)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (44)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (46)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (47)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (48)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (49)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (50)
<223> n equals a,t,g, or c

<220>
<221> misc_feature

<222> (51)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (52)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (53)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (54)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (55)
<223> n equals a,t,g, or c

<400> 33
agtcccatcg atgagcaacc tcactcttgt gtgcatcnnn nnnnnnnnnn nnnnn   55

<210> 34
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Stanniocalcin signal peptide

<400> 34
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Leu Val Ile Ser Ala Ser
 1   5   10   15

Ala

<210> 35
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Synthetic signal peptide

<400> 35
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu
 1   5   10   15

Trp Ala Pro Ala Arg Gly
             20

<210> 36
<211> 402
<212> DNA

22

<213> Homo sapiens

<400> 36
gctccaactt cttcttctac taagaagact caattgcaat tggaacactt gttgttggac 60
ttgcaaatga tcttaaacgg tataaacaac tataaaaacc caaagttgac tagaatgttg 120
actttcaagt tctacatgcc aaagaaagct actgaattga agcacttgca atgtttggaa 180
gaagaattga agccattgga agaagttttg aacttggctc aatctaagaa cttccacttg 240
agaccaagag atttgatttc taacattaac gttattgttt tggaattgaa gggttctgaa 300
actactttta tgtgcgagta cgcagacgaa actgctacta tcgttgagtt cttaaatagg 360
tggatcactt tctgccaatc tattatttct actttgacat aa 402

23